STEIC Brotechnology Systems Branch RAW-SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 4.2.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street. Alexandria, VA 22314

Revised 01/24/05

Rair Sequence Listing Ercor Summarye

ERROR DETECTE	
ATTN: NOW BIN F	SUGGESTED CORRECTION SERIAL NUMBER: 0532;787
70.80	CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS WHICH WERE INSERTED BY PTO SOFTWARE mines The numberical at the end of each line "wrapped" down to the next line. The
Wrapped N	ucloics The numberfiext at the end of each line "wrapped" down to the next line. This may occur if your file prevent "wrapping."
· ·····	was schieved in a word processor after creating is Please adjust some This may occur if your Gi
INVEND LINE	Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
)_Misaliened A	mino The number:
Numbering	The numbering under each 5" amino acid is misaligned. Do not use tab codes between numbers:
Non-ASCII	. The submitted file was a second and a second a second and a second a
••	The submitted file was not saved in ASCII(DOS) less, as required by the Sequence Rules. Please
SVariable Leng	th Sequence(s)
	th Sequence(s) contain n's or X22's representing more than one visidue. Per Sequence Rules, residue having variable leaves a langue residue. Please present the maximum variable leaves.
	each n or X22 can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. A "bug" in Patentin version 2.0.
CPatentin 2.0	A "bug" in Patentle wasting
· "bug"	acquences(s)
	previously coded nucleic acid sequence. Please manually copy the relevant <220>-<221> section to be missing from animo acid the subsequent amino acid sequence. Please manually copy the relevant <220>-<221> section to Artificial or Unknown and sequence. This applies to the manualtory <220>-<221>
•	the subsequent amino acid sequence. Please manually copy the relevant <220>-<223> section to Artificial or Unknown sequences. This applies to the manualtory <220>-<223> sections for
Skipped Sequen	con Control sequences.
(OLD RULES)	
	(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown) (4) SEQUENCE CHARACTERISTICS (Do not need to be seen to be shown)
	TO THE COURT OF TH
	This sequence is intentionally stipped
	Picase also adjust the "ful NIMOED OF STA
8 Skipped Sequence	Please also adjust the "(ii) NUMBER OF SEQUENCES response to include the stapped sequences.
(NEW RULES)	Sequence(s)
"Use of n's or Xaa's	Use of n's and/or Y and
(NEW RULES)	Use of n's and/or X22's have been dejected in the Sequence Listing
. •	fer 1 823 of Sequence Rules, use of <220 + <221 + is MANDA TORY if n's or Xaa's are present In <220> to <223> section, please capitain location of n or Xaa, and which see
10 Invalid < 213;	Per 1 823 of Seguence 20 .
Response	Per 1 82) of Sequence Rules, the only valid <213+ responses are. Unknown, Artificial Sequence in section is required when <213+ responses to Unknown, Artificial Sequence in Artificial Sequence.
	is Adificial Seducuce
11- Usc of <110.	Sequencely
	Use of (550) to (555) is MANDY LOKE, if (511) "Originism, reshouse it "Adige the reshouse; "Only now". Lieste explain to the (550) I cannot and associated uninteric identifiers and reshouse;
	Use of <220> to <223> is MANDA TORY if <211> "Organism" response is "Artificial Sequence" or "Security Control of Control
1) '0	00/01/1998, Vol 63, No. 104 pp. 29631-121 (S.
"pne" Laicutlu 5'0	Please do not use "Copy to Dist" (unestable 10)
•	resulting in missing — a distriction of Patentin version 2.0. Thus
11	File Manager" or any other mount measured on raw sequence
Misusc of NX11	"n" can only represent a single nucleotide: "X22" can only represent a single amino acid
	acticolide: "X23" can only represent a single amino acid

AMC - Diotechnology Systems Dranch - 09/09/2003



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/532,787

DATE: 05/10/2005 TIME: 13:40:43

Input Set : A:\Sequence 27353-514 US1.txt Output Set: N:\CRF4\05102005\J532787.raw

- 3 <110> APPLICANT: Sense Therapeutic Limited
- 5 <120> TITLE OF INVENTION: ENZYME ARRAY AND ASSAY
- 7 <130> FILE REFERENCE: 27353-514 US1
- C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/532,787
- C--> 10 <141> CURRENT FILING DATE: 2005-04-25
 - 12 <150> PRIOR APPLICATION NUMBER: GB 0311946.8
 - 13 <151> PRIOR FILING DATE: 2003-05-23
 - 15 <150> PRIOR APPLICATION NUMBER: PCT/EP02/14859
 - 16 <151> PRIOR FILING DATE: 2002-12-20
 - 18 <150> PRIOR APPLICATION NUMBER: GB 0224872.2
 - 19 <151> PRIOR FILING DATE: 2002-10-25
 - 21 <160> NUMBER OF SEQ ID NOS: 17
 - 23 <170> SOFTWARE: PatentIn version 3.2

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

- 25 <210> SEQ ID NO: 1
- 26 <211> LENGTH: 15
- 27 <212> TYPE: PRT
- 28 <213> ORGANISM: Artificial
- 30 <220> FEATURE:
- 31 <223> OTHER INFORMATION: Peptide
- 33 <400> SEQUENCE: 1
- a Leu'Ala Arg Arg Arg 35 Ala Met Ala Arg Ala Ala Ser Ala Ala A
- E--> 36 1 5
 - 39 <210> SEQ ID NO: 2
 - 40 <211> LENGTH: 12
 - 41 <212> TYPE: PRT
 - 42 <213> ORGANISM: Artificial
 - 44 <220> FEATURE:
 - 45 <223> OTHER INFORMATION
 - 47 <400> SEQUENCE: 2
 - 49 Glu Ala Lie Tyr Ala Ala Pro Phe Ala Lys Lys Ly
- E--> 50 1 5 1/8
 - 53 <210> SEQ ID NO: 3
 - 54 <211> LENGTH: 7
 - 55 <212> TYPE: PRT
 - 56 <213> ORGANISM: Artificial
 - 58 <220> FEATURE:
 - 59 <223> OTHER INFORMATION: Peptide
 - 61 <400> SEQUENCE: 3
 - 63 Leu Arg Arg Ala Ser Leu Gly

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on error Summary Sheet.

DATE: 05/10/2005

TIME: 13:40:43

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Input Set : A:\Sequence 27353-514 US1.txt
                    Output Set: N:\CRF4\05102005\J532787.raw
E--> 64 1 5
    67 <210> SEQ ID NO: 4
    68 <211> LENGTH: 13
    69 <212> TYPE: PRT
    72 <213> ORGANISM: Artificial
                                                                           See
item
    75 <223 > OTHER INFORMATION: (Peptid) SAME error
    74 <220> FEATURE:
    77 <400> SEQUENCE: 4
    79 Lys Lys Ser Arg Gly Asp Tyr Met Thr Met Gln Ile Gly 80 1 8 10 5
E--> 80 1 &
    82 <210> SEQ ID NO: 5
    83 <211> LENGTH: 10
    84 <212> TYPE: PRT
    85 <213> ORGANISM: Artificial
                                                                        on error
Summany
Sheet.
    87 <220> FEATURE:
    88 <223> OTHER INFORMATION: Peptide SAME COV
    90 <400> SEQUENCE: 5
    92 Lys Lys Leu Asn Arg Thr Leu Ser Val Ala
93 1 8 10 5
E--> 93 1 🖋
    96 <210> SEQ ID NO: 6
    97 <211> LENGTH: 23
    98 <212> TYPE: PRT
    99 <213> ORGANISM: Artificial
    102 <223 > OTHER INFORMATION: PEPTIDE SAME ETTOR
    104 <400> SEQUENCE: 6
    106 Lys Lys Val Ser Arg Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro
E--> 107 1 8 10 15
    110 Glu Asn Leu Asn Arg Pro Arg
E--> 111 20 20
    114 <210> SEQ ID NO: 7
    115 <211> LENGTH: 14
    116 <212> TYPE: PRT
    117 <213> ORGANISM: Artificial
    119 <220> FEATURE:
    120 <223 > OTHER INFORMATION: Peptide Same es
    122 <400> SEOUENCE: 7
    124 Lys Arg Arg Arg Ala Leu Ser Val Ala Ser Leu Pro Gly Leu
                  10
E--> 125 1 5
    128 <210> SEQ ID NO: 8
    129 <211> LENGTH: 10
    130 <212> TYPE: PRT
    131 <213> ORGANISM: Artificial
    133 <220> FEATURE:
    134 <223 > OTHER INFORMATION: PEPTIDE SAME ENTO
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/532,787

136 <400> SEQUENCE: 8

142 <210> SEQ ID NO: 9

20

E--> 139 1 -8

138 Arg Arg Arg Asp Asp Asp Ser Asp Asp Asp

```
DATE: 05/10/2005 SAME
TIME: 13:40:43 EPPOPS
                     PATENT APPLICATION: US/10/532,787
                     Input Set : A:\Sequence 27353-514 US1.txt
                     Output Set: N:\CRF4\05102005\J532787.raw
     143 <211> LENGTH: 15
     144 <212> TYPE: PRT
     145 <213> ORGANISM: Artificial
     147 <220> FEATURE:
     148 <223> OTHER INFORMATION: (Peptid)
     150 <400> SEQUENCE: 9
     152 Lys Val Glu Lys Tle Cly Glu Gly Thr Tyr Gly Val Val Tyr Lys
E--> 158 1 5
                  10
     155 <210> SEQ ID NO:
     156 <211> LENGTH: 26
     157 <212> TYPE: PRT
     158 <213> ORGANISM: Artificial
     160 <220> FEATURE:
     161 <223> OTHER INFORMATION: (Peptide)
     163 <400> SEQUENCE: 10
     165 Tyr Arg Arg Ala Ala Val Pro Pro Ser Pro Ser Leu Ser Arg His Ser
E--> 166 1 5 10
                            15
     16 Ser Pro His Gln Ser Glu Asp Glu Glu Glu
E--> 170 20
                  25
     173 <210> SEQ ID NO: 11
     174 <211> LENGTH: 14
     175 <212> TYPE: PRT
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     178 <220> FEATURE:
     179 <223> OTHER INFORMATION: (Peptide
     181 <400> SEQUENCE: 11
     183 Lys Lys Eys Ser Pro Gly Glu Tyr Val Asn Ile Glu Phe Gly
E--> 184 1 5
                  10
     187 <210> SEQ ID NO: 12
     188 <211> LENGTH: 13
     189 <212> TYPE: PRT
     190 <213> ORGANISM: Artificial
     192 <220> FEATURE:
     193 <223> OTHER INFORMATION: Reptide
     195 <400> SEQUENCE: 12
     197 Gly Arg Pro Arg Thr Ser Ser Phe Ala Glu Gly Lys Lys
E--> 198(1 5
     201 <210> SEQ ID NO: 13
     202 <211> LENGTH: 9
     203 <212> TYPE: PRT
     204 <213> ORGANISM: Artificial
    206 <220> FEATURE:
     207 <223> OTHER INFORMATION: Peptide
     209 <400> SEQUENCE: 13
     211 Lys Lys Arg Asn Arg Thr Leu Thr Val
E--> 212 1 5
     215 <210> SEQ ID NO: 14
     216 <211> LENGTH: 39
     217 <212> TYPE: PRT
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RAW SEQUENCE LISTING

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/532,787

DATE: 05/10/2005

TIME: 13:40:43

Input Set: A:\Sequence 27353-514 US1.txt
Output Set: N:\CRF4\05102005\J532787.raw



RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/10/2005 PATENT APPLICATION: US/10/532,787 TIME: 13:40:44

Input Set : A:\Sequence 27353-514 US1.txt
Output Set: N:\CRF4\05102005\J532787.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17

VERIFICATION SUMMARY DATE: 05/10/2005 PATENT APPLICATION: US/10/532,787 TIME: 13:40:44

Input Set : A:\Sequence 27353-514 US1.txt
Output Set: N:\CRF4\05102005\J532787.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:36 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1 L:50 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2 L:64 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3 L:80 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4 L:93 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5 L:107 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6 M:332 Repeated in SeqNo=6 L:125 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7 L:139 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8 L:153 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9 L:166 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10 M:332 Repeated in SeqNo=10 L:184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11 L:198 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12 L:212 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13 L:226 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14 M:332 Repeated in SeqNo=14 L:247 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15 L:260 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16 L:274 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17